

05/90
1108

Page 1 of 7

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/973,322

DATE: 10/30/2001
TIME: 15:33:49

Input Set : A:\SEQLISTDYOU17001CP1.TXT
Output Set: N:\CRF3\10302001\I973322.raw

ENTERED

2.

4 <110> APPLICANT: Hope, Ralph Graham
5 McLauchlan, John
7 <120> TITLE OF INVENTION: VIRAL THERAPEUTICS
10 <130> FILE REFERENCE: DYOUN17.001CP1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/973,322
C--> 12 <141> CURRENT FILING DATE: 2001-10-09
12 <150> PRIOR APPLICATION NUMBER: US 09/201,916
13 <151> PRIOR FILING DATE: 1998-12-01
15 <150> PRIOR APPLICATION NUMBER: GB 9825951.8
16 <151> PRIOR FILING DATE: 1998-11-26
18 <160> NUMBER OF SEQ ID NOS: 20
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 630
24 <212> TYPE: DNA
25 <213> ORGANISM: Hepatitis C Virus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (43)...(630)
31 <400> SEQUENCE: 1
32 ggtgcttgcg agtgcccccgg gaggtctcggt agaccgtgca cc atg agc acg aat 54
33 1 Met Ser Thr Asn
34 5 10 15 20 102
36 cct aaa cct caa aga aaa acc aaa cgt aac acc aac cgt cgc cca cag 102
37 Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn Arg Arg Pro Gln
38 5 10 15 20
40 gac gtt aag ttc ccg ggt ggc ggt cag atc gtt ggt gga gtt tac ttg 150
41 Asp Val Lys Phe Pro Gly Gly Gln Ile Val Gly Gly Val Tyr Leu
42 25 30 35
44 ttg ccg cgc agg ggc cct aga ttg ggt gtg cgc gcg acg agg aag act 198
45 Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala Thr Arg Lys Thr
46 40 45 50
48 tcc gag cgg tcg caa cct cga ggt aga cgt cag cct atc ccc aag gca 246
49 Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala
50 55 60 65
52 cgt cgg ccc aag ggc agg aac tgg gct cag ccc ggg tat cct tgg ccc 294
53 Arg Arg Pro Lys Gly Arg Asn Trp Ala Gln Pro Gly Tyr Pro Trp Pro
54 70 75 80
56 ctc tat ggc aat gag ggt tgc ggg tgg gcg gga tgg ctc ctg tcc ccc 342
57 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu Ser Pro
58 85 90 95 100
60 agt ggc tct cgg cct agt tgg ggc ccc aac gac ccc cga cgt agg tgc 390
61 Ser Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro Arg Arg Ser
62 105 110 115
64 cgc aat ttg ggt aag gtc atc gat acc ctt acg tgc ggc ttc gtc gat 438
65 Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys Gly Phe Val Asp
66 120 125 130

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68 ctc atg ggg tac ata ccg ctc gtc ggc gcc cct ctt aga ggc gct gcc 486
69 Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu Arg Gly Ala Ala
70      135           140           145
72 agg gcc ctg gcg cat ggc gtc cgg gtt ctg gaa gac ggt gtg aac tat 534
73 Arg Ala Leu Ala His Gly Val Arg Val Leu Glu Asp Gly Val Asn Tyr
74      150           155           160
76 gca aca ggt aac ctt cct ggt tgc tct ttc tct atc ttc ctt ctg gcc 582
77 Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala
78 165           170           175           180
80 ctg ctc tct tgc ctg act gtg ccc gct tca gcc tac caa gtg cgc aac 630
81 Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala Tyr Gln Val Arg Asn
82      185           190           195
86 <210> SEQ ID NO: 2
87 <211> LENGTH: 60
88 <212> TYPE: DNA
89 <213> ORGANISM: Hepatitis C Virus
91 <220> FEATURE:
92 <221> NAME/KEY: CDS
93 <222> LOCATION: (1)...(60)
94 <223> OTHER INFORMATION: Corresponds to aa 125 to 144 of SEQ ID. No. 1
96 <400> SEQUENCE: 2
97 acc ctt acg tgc ggc ttc gtc gat ctc atg ggg tac ata ccg ctc gtc 48
98 Thr Leu Thr Cys Gly Phe Val Asp Leu Met Gly Tyr Ile Pro Leu Val
99 1           5           10           15
101 ggc gcc cct ctt           60
102 Gly Ala Pro Leu
103      20
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 18
108 <212> TYPE: DNA
109 <213> ORGANISM: Hepatitis C Virus
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (1)...(18)
114 <223> OTHER INFORMATION: Corresponds to aa 161-166 of SEQ ID. No. 1
116 <400> SEQUENCE: 3
117 ggt gtg aac tat gca aca           18
118 Gly Val Asn Tyr Ala Thr
119 1           5
122 <210> SEQ ID NO: 4
123 <211> LENGTH: 1900
124 <212> TYPE: DNA
125 <213> ORGANISM: Human
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (1)...(1900)
130 <223> OTHER INFORMATION: n = A,T,C or G
132 <400> SEQUENCE: 4
133 cgttccggg acgcggccgc tcttcgcctt tcgctgcagt ccgtcgattt ctttctccag 60

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DATE: 10/30/2001

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Input Set : A:\SEQLISTDYOU17001CP1.TXT

Output Set: N:\CRF3\10302001\I973322.raw

134 gaagaaaaat ggcacccgtt gcagttgatc cacaaccgag tgggttgact cgggtggta 120
 135 acctggccctt ggtgagtc acgtatgacc tcattgtcctc agcctatctc agtacaaagg 180
 136 accagtatcc ctacctgaag tctgtgtgt agatgscaga gaacgggtgt aagaccatca 240
 137 cctccgtggc catgaccagt gctctgccc tcattccagaa gctagagccg caaattgcag 300
 138 ttgccgatac ctatgcctgt aaggggctag acaggattga ggagagactg cctattctga 360
 139 atcagccatc aactcagatt gttgccaaatg ccaaaggcgac tggacttggg gcaaaagatg 420
W--> 140 ctgtgacgac tactgtgact gggggccaagg attctgtngc cagcacgatc acaggggtga 480
 141 tggacaagac caaaggggca gtgactggca gtgtggagaa gaccaagtct gtggtcagt 540
 142 gcagcattaa cacagtctt gggagtcgga tgatgcgt cgtgacgt ggcgttagaaa 600
 143 atgcactcac caaatcagag ctgttggtag aacagtacat ccctctact gaggaagaac 660
 144 tagaaaaaga agcaaaaaaa gttgaaggat ttgatcttgt tcagaaggca agtattatgt 720
 145 ttagactggg atccctgtct accaagcttc actccctgtc ctaccacgc gctctcagca 780
 146 gggtaaaaga agctaagcaa aaaagccaa acaccatttc tcagctccat tctactgttc 840
 147 acctgattga atttgcagg aagaatgtgt atagtccaa tcagaaaatt cagatgctc 900
 148 aggataagct ctacccatca tggtagagt gggaaaggag cattggatat gatgatactg 960
 149 atgagtcctt ctgtgctgag cacattgatg cacgtactct tgcaatttgc cgcaacacta 1020
 150 ctcagcactt ccagaccacg tgccacaccc tcctgtccaa catccaagggt gtaccacaga 1080
 151 acatccaaga tcaagccaa acatggggg tgatggcagg cgacatctac tcagtttcc 1140
 152 gcaatgctgc ctcccttaaa gaagtgtctg acacccctt cacttcttagc aaggggcagc 1200
 153 tgcagaaaat gaaggaaatct ttagatgacg tgatggatta tcttgttaac aacacgcgg 1260
 154 tcaactggct ggttaggtccc ttttatctc agctgactga gtctcagaat gctcaggacc 1320
 155 aaggtgcaga gatggacaag acgagccagg agacccagcg atctgagcat aaaactcatt 1380
 156 aaacctgccc ctatcactag tgcattgtt ggcacagacg atgacacatt ttgttatgtt 1440
 157 gaaattaaact tgctaggcaa ccctaaattt ggaagcaagt agcttagata aagccctca 1500
 158 attgttagttt tttccagctg aattaagagc tttaaagttt ctggcattag cagatgattt 1560
 159 ctgttccactt ggttaaaaaaa gaatgatagg cttgtcagag cctatagcca gaactcagaa 1620
 160 aaaattcaaa tgcacttatg ttcttattt atggccattt tggtgcctt gttactgttt 1680
 161 gtattgaata aaaacatctt catgtggct gggtagaaa ctgggtctg ctctgggttg 1740
 162 atctgaaaag gcgttccac tgctttatct catgtgctt gcttgtaaaa ctgtatttt 1800
 163 gtttttcatt tctcaaatag gaatactacc tttgaattca ataaaatca ctgcaggata 1860
W--> 164 gaccagttta gnageaaaca nncangtaca cnnaaganac 1900
 166 <210> SEQ ID NO: 5
 167 <211> LENGTH: 437
 168 <212> TYPE: PRT
 169 <213> ORGANISM: Human
 171 <220> FEATURE:
 172 <221> NAME/KEY: VARIANT
 173 <222> LOCATION: (1)...(437)
 174 <223> OTHER INFORMATION: Xaa = Any Amino Acid
 176 <400> SEQUENCE: 5
 177 Met Ala Ser Val Ala Val Asp Pro Gln Pro Ser Val Val Thr Arg Val
 178 1 5 10 15
 179 Val Asn Leu Pro Leu Val Ser Ser Thr Tyr Asp Leu Met Ser Ser Ala
 180 20 25 30
 181 Tyr Leu Ser Thr Lys Asp Gln Tyr Pro Tyr Leu Lys Ser Val Cys Glu
 182 35 40 45
W--> 183 Met Xaa Glu Asn Gly Val Lys Thr Ile Thr Ser Val Ala Met Thr Ser
 184 50 55 60
 185 Ala Leu Pro Ile Ile Gln Lys Leu Glu Pro Gln Ile Ala Val Ala Asp

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/973 322

DATE: 10/30/2001

TIME: 15:33:49

Input Set : A:\SEOLIST\TRYOUT\Z001CB1.TVM

Output Set: N:\CBF3\10302001\t973322.nam

186	65	70	75	80
187	Tyr Ala Cys Lys Gly Leu Asp Arg Ile Glu Glu Arg Leu Pro Ile			
188	85	90		95
189	Leu Asn Gln Pro Ser Thr Gln Ile Val Ala Asn Ala Lys Gly Ala Val			
190	100	105	110	
191	Thr Gly Ala Lys Asp Ala Val Thr Thr Val Thr Gly Ala Lys Asp			
192	115	120	125	
193	Ser Val Ala Ser Thr Ile Thr Gly Val Met Asp Lys Thr Lys Gly Ala			
194	130	135	140	
195	Val Thr Gly Ser Val Glu Lys Thr Lys Ser Val Val Ser Gly Ser Ile			
196	145	150	155	160
197	Asn Thr Val Leu Gly Ser Arg Met Met Gln Leu Val Ser Ser Gly Val			
198	165	170	175	
199	Glu Asn Ala Leu Thr Lys Ser Glu Leu Leu Val Glu Gln Tyr Leu Pro			
200	180	185	190	
201	Leu Thr Glu Glu Glu Leu Glu Lys Glu Ala Lys Lys Val Glu Gly Phe			
202	195	200	205	
203	Asp Leu Val Gln Lys Pro Ser Tyr Tyr Val Arg Leu Gly Ser Leu Ser			
204	210	215	220	
205	Thr Lys Leu His Ser Arg Ala Tyr Gln Gln Ala Leu Ser Arg Val Lys			
206	225	230	235	240
207	Glu Ala Lys Gln Lys Ser Gln Gln Thr Ile Ser Gln Leu His Ser Thr			
208	245	250	255	
209	Val His Leu Ile Glu Phe Ala Arg Lys Asn Val Tyr Ser Ala Asn Gln			
210	260	265	270	
211	Lys Ile Gln Asp Ala Gln Asp Lys Leu Tyr Leu Ser Trp Val Glu Trp			
212	275	280	285	
213	Lys Arg Ser Ile Gly Tyr Asp Asp Thr Asp Glu Ser His Cys Ala Glu			
214	290	295	300	
215	His Ile Glu Ser Arg Thr Leu Ala Ile Ala Arg Asn Leu Thr Gln Gln			
216	305	310	315	320
217	Leu Gln Thr Thr Cys His Thr Leu Leu Ser Asn Ile Gln Gly Val Pro			
218	325	330	335	
219	Gln Asn Ile Gln Asp Gln Ala Lys His Met Gly Val Met Ala Gly Asp			
220	340	345	350	
221	Ile Tyr Ser Val Phe Arg Asn Ala Ala Ser Phe Lys Glu Val Ser Asp			
222	355	360	365	
223	Ser Leu Leu Thr Ser Ser Lys Gly Gln Leu Gln Lys Met Lys Glu Ser			
224	370	375	380	
225	Leu Asp Asp Val Met Asp Tyr Leu Val Asn Asn Thr Pro Leu Asn Trp			
226	385	390	395	400
227	Leu Val Gly Pro Phe Tyr Pro Gln Leu Thr Glu Ser Gln Asn Ala Gln			
228	405	410	415	
229	Asp Gln Gly Ala Glu Met Asp Lys Ser Ser Gln Glu Thr Gln Arg Ser			
230	420	425	430	
231	Glu His Lys Thr His			
232	435			
235	<210> SEQ ID NO: 6			
236	<211> LENGTH: 31			

RAW SEQUENCE LISTING

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Input Set : A:\SEQLISTDYOU17001CP1.TXT
 Output Set: N:\CRF3\10302001\I973322.raw

```

237 <212> TYPE: PRT
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: branched peptide containing residues 5-27 of HCV
242 core protein
244 <221> NAME/KEY: VARIANT
245 <222> LOCATION: (1)...(31)
246 <223> OTHER INFORMATION: Xaa = Ala or Pro at position 1, and Ile or Asn at
247 position 12
249 <400> SEQUENCE: 6
W--> 250 Xaa Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Xaa Arg Arg Pro Gln
251 1 5 10 15
252 Asp Val Lys Phe Pro Gly Gly Lys Lys Lys Lys Lys Lys Ala
253 20 25 30
256 <210> SEQ ID NO: 7
257 <211> LENGTH: 11
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
263 protein deletion plasmids
265 <400> SEQUENCE: 7
266 gctgagatct a 11
268 <210> SEQ ID NO: 8
269 <211> LENGTH: 29
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
275 protein deletion plasmids
277 <400> SEQUENCE: 8
278 gtaacccttcc tggttgctct tgagatcta 29
280 <210> SEQ ID NO: 9
281 <211> LENGTH: 17
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
287 protein deletion plasmids
289 <400> SEQUENCE: 9
290 gtaacccttgc agatcta 17
292 <210> SEQ ID NO: 10
293 <211> LENGTH: 18
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: oligonucleotides used to construct HCV core
299 protein deletion plasmids
301 <400> SEQUENCE: 10

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/973,322

DATE: 10/30/2001

TIME: 15:33:50

Input Set : A:\SEQLISTDYOU17001CP1.TXT
Output Set: N:\CRF3\10302001\I973322.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:164 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6